SEQUENCE LISTING

<110> McCarthy, Sean A. Holtzman, Douglas A. Goodearl, Andrew D.J. <120> NOVEL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC AND OTHER USES <130> 07334-325001 <150> US 09/128,709 <151> 1998-08-04 <150> US 60/054,645 <151> 1997-08-04 <150> US 09/130,491 <151> 1998-08-06 <150> US 60/054,966 <151> 1997-08-06 <150> US 60/058,108 <151> 1997-09-05 <150> US 09/388,280 <151> 1999-09-01 <150> US 09/388,279 <151> 1999-09-01 <160> 14 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 3147 <212> DNA <213> Homo sapiens <220> <221> CDS <222> (3)...(1826) <400> 1 cc acg cgt ccg atc ttg gtc atc cac gat gaa cag aag ggg ccg gaa 47 Thr Arg Pro Ile Leu Val Ile His Asp Glu Gln Lys Gly Pro Glu gtg acc tcc aat gct gcc ctc act ctg cgg aac ttt tgc aac tgg cag 95 Val Thr Ser Asn Ala Ala Leu Thr Leu Arg Asn Phe Cys Asn Trp Gln 20 25

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143

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					aga Arg											191
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					gat Asp 85											287
					gtg Val											335
					ggt Gly											383
					gac Asp											431
tac Tyr	atg Met 145	att Ile	aca Thr	tca Ser	ttt Phe	ctg Leu 150	gat Asp	aat Asn	ggt Gly	cat His	ggg Gly 155	gaa Glu	tgt Cys	ttg Leu	atg Met	479
gac Asp 160	aag Lys	cct Pro	cag Gln	aat Asn	ccc Pro 165	ata Ile	cag Gln	ctc Leu	cca Pro	ggc Gly 170	gat Asp	ctc Leu	cct Pro	ggc Gly	acc Thr 175	527
tcg Ser	tac Tyr	gat Asp	gcc Ala	aac Asn 180	cgg Arg	cag Gln	tgc Cys	cag Gln	ttt Phe 185	aca Thr	ttt Phe	gly ggg	gag Glu	gac Asp 190	tcc Ser	575
aaa Lys	cac His	tgc Cys	ccc Pro 195	gat Asp	gca Ala	gcc Ala	agc Ser	aca Thr 200	tgt Cys	agc Ser	acc Thr	ttg Leu	tgg Trp 205	tgt Cys	acc Thr	623
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	cac aac gag ttt His Asn Glu Phe 325			
	tgg att ccc aag Trp Ile Pro Lys 340			
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gcc atc aaa gct Ala Ile Lys Ala 465	gct gat ggc aca Ala Asp Gly Thr 470	Tyr Ile Leu A	aat ggt gac tac Asn Gly Asp Tyr 175	act 1439 Thr
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Asp	Arg	Ala	Val	Leu 50	Cys	His	Arg	Lys	Arg 55	Phe	Val	Ala	Val	Pro 60	Glu	
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Gly	Ile	Pro	Thr 65	Glu	Thr	Arg	Leu	Leu 70	Asp	Leu	Gly	Lys	Asn 75	Arg	Ile	
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												agc Ser				505
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cat His	gag Glu	ctg Leu	ctc Leu	cgg Arg	ctg Leu	cag Gln	gag Glu	atc Ile	cag Gln	ctg Leu	gtg Val	ggc Gly	gly aaa	cag Gln	ctg Leu	1081

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aac ttc aac cgg Asn Phe Asn Arg 385	Gln Gln Pro	acg tgc gc Thr Cys Al 390	cc acg ccc gag tt La Thr Pro Glu Ph 39	ne Val Gln
ggc aag gag tto Gly Lys Glu Phe 400	aag gac ttc Lys Asp Phe	cct gat gt Pro Asp Va 405	ng cta ctg ccc as al Leu Leu Pro As 410	nc tac ttc 1369 on Tyr Phe
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His	Gly 210	Leu	Ile	Val	Leu	Arg 215	Leu	Arg	His	Leu	Asn 220	Ile	Asn	Ala	Ile
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	290		Pro			295					300				
305			Gln		310				_	315					320
			Ala	325		_			330					335	
			Gln 340					345					350		
		355	Glu				360					365		_	_
	370		Leu			375	_		_	_	380				
385			Pro		390					395			_	_	400
			Phe	405					410		_			415	_
			Ile 420	_	_	_	-	425					430	_	
		435	Val				440					445			
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465			Leu		470					475					480
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                         Met Gln Val Ser Glu Arg Met Leu Ala Gly
ggt atg aga age atg eec age eec ete etg gee tge tgg eag eec ate
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Gly Met Arg Ser Met Pro Ser Pro Leu Leu Ala Cys Trp Gln Pro Ile
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		ctg Leu						-								448
		cgc Arg 45														496
_		cgc Arg													_	544
		gac Asp														592
		agc Ser														640
	_	gcc Ala		_			-							_		688
	_	999 Gly 125	_	_	_		_	_	_			_	_		_	736
		ggc														784
		atc Ile														832
		gag Glu			_		_							_	-	880
		ggc Gly														928
		tcc Ser 205														976
		cgg Arg														1024
		agg Arg														1072
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Ser Ala Gln Asp Arg Ala Val Leu Cys His Arg Lys Arg Phe Val Ala
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Val Pro Glu Gly Ile Pro Thr Glu Thr Arg Leu Leu Asp Leu Gly Lys
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Asn Arg Ile Lys Thr Leu Asn Gln Asp Glu Phe Ala Ser Phe Pro His
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Leu Glu Glu Leu Glu Leu Asn Glu Asn Ile Val Ser Ala Val Glu Pro
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Gly Ala Phe Asn Asn Leu Phe Asn Leu Arg Thr Leu Gly Leu Arg Ser
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Asn Arg Leu Lys Leu Ile Pro Leu Gly Val Phe Thr Gly Leu Ser Asn
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Leu Thr Lys Leu Asp Ile Ser Glu Asn Lys Ile Val Ile Leu Leu Asp
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Tyr Met Phe Gln Asp Leu Tyr Asn Leu Lys Ser Leu Glu Val Gly Asp
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                165
Asn Asp Leu Val Tyr Ile Ser His Arg Ala Phe Ser Gly Leu Asn Ser
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                                                    190
Leu Glu Gln Leu Thr Leu Glu Lys Cys Asn Leu Thr Ser Ile Pro Thr
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                            200
Glu Ala Leu Ser His Leu His Gly Leu Ile Val Leu Arg Leu Arg His
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                                            220
Leu Asn Ile Asn Ala Ile Arg Asp Tyr Ser Phe Lys Arg Leu Tyr Arg
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Met Ala Gly Ser

ccg Pro 5	ctg Leu	ctc Leu	tgc Cys	gly ggg	ccg Pro 10	cgg Arg	gcc Ala	gly aaa	ggc	gtc Val 15	ggc Gly	att Ile	ttg Leu	gtg Val	ctg Leu 20	165
ctg Leu																213
gtg Val	aag Lys	gag Glu	ccc Pro 40	cgc Arg	agt Ser	ctg Leu	agc Ser	gca Ala 45	gca Ala	tcc Ser	gcg Ala	ccc Pro	ttg Leu 50	gtt Val	gag Glu	261
acg Thr				ctc Leu												309
gcg Ala																357
gcc Ala 85				gaa Glu												405
				gtc Val 105												453
				ccg Pro												501
				gcc Ala												549
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				ctg Leu							tga	ggta	ctt ·	gcta	gggcgg	650
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